

	peptide sequence	residue change	FPKM	predicted likelihood of presentation (-10logOdds, hmMHC)	median predicted affinity (nM, IEDB)	neoepitope ratio
Hmgb1	FFLFCSEYRPKIKSEHPGLSIGDVAKK	G115S	1586.62	28.52	3333	1.19
Itgb1	DDCWYFYFTYSVNGYNEAIVHVVETPDCP	N710Y	795.18	26.10	769	20.98
Akr1a1	NETEIGEALKESVSGKAVPREELFVT	G65V	246.72	26.20	3333	1.74
Zzz3	VVDHDADFQGAKPACRCLLDDCEKRE	R168P	186.24	27.62	323	5.92
Eif4a3	PQKERESIMKEFRSAASRVLISTDVWAR	G326A	166.25	26.45	69	2.11
Eif4g1	EEGGEAESEKGGGEYVPLDSTPVPAQLS	D480Y	152.42	26.02	370	1.91
Txnrd1	CPNCCWFPGFLPPFPRPPHVPRVLLRG	V41F	124.90	27.66	81	1.00
Rfc1	TCPRGLDVKETHGSRSSNKEECLLWVD	N559S	113.90	27.32	10000	1.86
Bbx	TSHPDAPSKQCQASPLFQFAEISSSTSQ	A268P	70.47	25.26	161	1.34
Senp6	MLSNNKKLSESTAATALCSGTVVHGRR	A121P	64.86	25.99	400	1.70
Nemf	FLFKVDESCVWRHRCERKVRVPDEDEME	G667C	30.87	33.71	20000	0.99
Nrg1	SLEVAPAFRLAESSTNPAGRFSTQEEL	R697S	22.11	25.29	385	2.96
Fstl4	KNLKEPPRGPAPTLGGPRRVLDRDGLF	W839L	17.79	24.93	714	3.65
Mpped1	VNASVCTVNYQPVNPPIVILLPTPRNS	D319L	17.33	26.35	86	2.28
Ube2c	YEDLRYKLSLEFPSVYPYNAPT VKFLTP	G88V	16.38	26.37	104	1.44
Lrrc37a	FASGKAAALKHPVRNAPSPKRNEARHS	D317V	11.70	28.10	82	1.37
Klhdc7a	RFVSKELKGFPAPGTLLPAVLTLPVP	R753P	10.90	24.80	625	7.99
Abcb1b	EMAIYAYYYTGIGAAVLIVAYIQVSLWC	G123A	7.71	27.62	128	1.50
Myo15	ARQGLGFGPEFGHSTPRPATSLARFKL	P555S	6.63	24.98	556	4.12
Pax9	GQAPNGLSAVSSFVSASSMAPYPTPAQV	P264S	5.79	25.83	105	3.22
Kif26b	TELPASKAQRNRSTAPT VTRSSSPSPA	P1008T	4.98	24.25	235	16.21
Cpa2	SGSFCVGVDPNRNCDANFGGPGASSNP	W167C	4.86	26.36	81	1.19
L3mbtl3	VKHFSWDKYLEETYSLPAPARAFKVKP	N458Y	4.06	23.76	74	9.38
ApoB	QLQVPLLGVLDLSSNVYSNLYNWSASY	T1360S	1.54	28.65	5000	1.35

**Supplemental Table 1: Characteristics of the screened predicted MHC class II neoantigens.** Sequences of mutant peptides identified in T3 sarcomas used in the screening experiments. The mutant amino acid in each peptide is indicated in red. Expression was estimated by mutant fragments per kilobase of transcript per million mapped reads (FPKM). Predicted peptide binding affinity was calculated using 1) hmMHC and 2) netMHCII and netMHCIIpan (IEDB).